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NEWS 7	DEC 21	IPC search and display fields enhanced in CA/CAplus with the IPC reform
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NEWS 18	FEB 22	Updates in EPFULL; IPC 8 enhancements added
NEWS 19	FEB 27	New STN AnaVist pricing effective March 1, 2006
NEWS 20	FEB 28	MEDLINE/LMEDLINE reload improves functionality
NEWS 21	FEB 28	TOXCENTER reloaded with enhancements
NEWS 22	FEB 28	REGISTRY/ZREGISTRY enhanced with more experimental spectral property data
NEWS 23	MAR 01	INSPEC reloaded and enhanced
NEWS 24	MAR 03	Updates in PATDPA; addition of IPC 8 data without attributes
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COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
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=> porcine or pig or swine or sow or sus
L1 1305869 PORCINE OR PIG OR SWINE OR SOW OR SUS

=> l1 and (array or microarray)
L2 2967 L1 AND (ARRAY OR MICROARRAY)

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L3 475 L2 AND (CDNA OR MRNA)

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PROCESSING COMPLETED FOR L4
L5 52 DUP REM L4 (42 DUPLICATES REMOVED)

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5 FILES SEARCHED...
L6 24 L5 AND PY<2004

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YOU HAVE REQUESTED DATA FROM 24 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 24 MEDLINE on STN
TI Cross-species hybridisation of **pig** RNA to human nylon **microarrays**.

L6 ANSWER 2 OF 24 MEDLINE on STN

TI Ascaris suum: **cDNA microarray** analysis of 4th stage larvae (L4) during self-cure from the intestine.

L6 ANSWER 3 OF 24 MEDLINE on STN
TI Leptin receptor-deficient Zucker (fa/fa) rat retards the development of **pig** serum-induced liver fibrosis with Kupffer cell dysfunction.

L6 ANSWER 4 OF 24 MEDLINE on STN
TI Complementary DNA macroarray analyses of differential gene expression in **porcine** fetal and postnatal **muscle**.

L6 ANSWER 5 OF 24 MEDLINE on STN
TI Development of a **porcine** skeletal **muscle cDNA microarray**: analysis of differential transcript expression in phenotypically distinct **muscles**.

L6 ANSWER 6 OF 24 MEDLINE on STN
TI Generation of expressed sequence tags from a normalized **porcine** skeletal **muscle cDNA** library.

L6 ANSWER 7 OF 24 MEDLINE on STN
TI The biology of somatotropin in adipose tissue growth and nutrient partitioning.

L6 ANSWER 8 OF 24 MEDLINE on STN
TI The GalR2 galanin receptor mediates galanin-induced jejunal contraction, but not feeding behavior, in the rat: differentiation of central and peripheral effects of receptor subtype activation.

L6 ANSWER 9 OF 24 MEDLINE on STN
TI Structure of tropomyosin at 9 angstroms resolution.

L6 ANSWER 10 OF 24 CABA COPYRIGHT 2006 CABI on STN
TI Cross-species hybridisation of **pig** RNA to human nylon **microarrays**.

L6 ANSWER 11 OF 24 CABA COPYRIGHT 2006 CABI on STN
TI The biology of somatotropin in adipose tissue growth and nutrient partitioning.

L6 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI Genes expressed in atherosclerotic tissue and their use in diagnosis and pharmacogenetics

L6 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI Identification of candidate genes and proteins related to human atherosclerosis susceptibility locus (ATHS) and genetic markers for atherosclerosis prediction

L6 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI Genes showing altered patterns of expression in multiple sclerosis and their diagnostic and therapeutic uses

L6 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI Novel pharmaceutical composition of interferon gamma or pirfenidone combined with molecular diagnostics for the improved treatment of interstitial lung diseases

L6 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI **Muscle**-specific F-box protein, atrogin-1, highly expressed during **muscle** atrophy, and compositions and methods for diagnosis and treatment of **muscle** wasting

L6 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

TI Development of a **porcine** skeletal **muscle cDNA microarray**: analysis of differential transcript expression in phenotypically distinct **muscles**

L6 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI Cell-specific gene expression profiles and algorithms for their construction and their uses for determining the phenotype of cells and distinguishing cell lines

L6 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
TI Identification of proacrosin binding protein sp32 precursor as a human cancer/testis antigen

L6 ANSWER 20 OF 24 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Leptin receptor-deficient Zucker (fa/fa) rat retards the development of **pig** serum-induced liver fibosis with Kupffer cell dysfunction.

L6 ANSWER 21 OF 24 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI A Comparison of **Porcine** Ocular Tissue Gene Expression by **Microarray** Analysis.

L6 ANSWER 22 OF 24 DISSABS COPYRIGHT (C) 2006 ProQuest Information and Learning Company; All Rights Reserved on STN
TI Molecular, genetic and physical mapping of the **porcine** genome

L6 ANSWER 23 OF 24 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN
TI Cross-species hybridisation of **pig** RNA to human nylon **microarrays**.

L6 ANSWER 24 OF 24 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN
TI Development of a **porcine** skeletal **muscle cDNA microarray**: Analysis of differential transcript expression in phenotypically distinct **muscles**.

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PROCESSING COMPLETED FOR L6
L7 24 DUP REM L6 (0 DUPLICATES REMOVED)

=> d l6 10, 1, 6, 21 ibib abs

L6 ANSWER 10 OF 24 CABA COPYRIGHT 2006 CABI on STN
ACCESSION NUMBER: 2004:172135 CABA
DOCUMENT NUMBER: 20043153082
TITLE: Cross-species hybridisation of **pig** RNA to human nylon **microarrays**
AUTHOR: Moody, D. E.; Zou, Z.; McIntyre, L.
CORPORATE SOURCE: Department of Animal Science, 1151 Lilly Hall, Purdue University, West Lafayette, IN 47907, USA. moodyd@purdue.edu; chenwei.tseng@mesanetworks.net; lmcintyre@purdue.edu
SOURCE: BMC Genomics, (**2002**) Vol. 3, No. 27, pp. (27 September 2002). 15 ref.
Publisher: BioMed Central Ltd. London
ISSN: 1471-2164
URL: http://www.biomedcentral.com/1471-2164/3/27/abstract
DOI: 10.1186/1471-2164-3-27
PUB. COUNTRY: United Kingdom
DOCUMENT TYPE: Journal

LANGUAGE: English
ENTRY DATE: Entered STN: 20041108
Last Updated on STN: 20041108

AB Background: The objective of this research was to investigate the reproducibility of cross-species **microarray** hybridization. Comparisons between same- and cross-species hybridizations were also made. Nine hybridizations between a single **pig** skeletal **muscle** RNA sample and three human **cDNA** nylon **microarrays** were completed. Three replicate hybridizations of two different amounts of **pig** RNA, and of human skeletal **muscle** RNA were completed on three additional **microarrays**. Results: Reproducibility of **microarray** hybridizations of **pig cDNA** to human **microarrays** was high, as determined by Spearman and Pearson correlation coefficients and a Kappa statistic. Variability among replicate hybridizations was similar for human and **pig** data, indicating the reproducibility of results were not compromised in cross-species hybridized. The concordance between data generated from hybridizations using **pig** and human skeletal **muscle** RNA was high, further supporting the use of human **microarrays** for the analysis of gene expression in the **pig**. No systematic effect of stripping and reusing nylon **microarrays** was found, and variability across **microarrays** was minimal. Conclusion: The majority of genes generated highly reproducible data in cross-species **microarray** hybridizations, although approximately 6% were identified as highly variable. Experimental designs that include at least three replicate hybridizations for each experimental treatment will enable the variability of individual genes to be considered appropriately. The use of cross-species **microarray** analysis looks promising. However, additional validation is needed to determine the specificity of cross-species hybridizations, and the validity of results.

L6 ANSWER 1 OF 24 MEDLINE on STN
ACCESSION NUMBER: 2003510296 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12354330
TITLE: Cross-species hybridisation of **pig** RNA to human nylon **microarrays**.
AUTHOR: Moody D E; Zou Z; McIntyre L
CORPORATE SOURCE: Department of Animal Science, 1151 Lilly Hall, Purdue University, West Lafayette, IN 47907, USA.. moodyd@purdue.edu
SOURCE: BMC genomics [electronic resource], **(2002 Sep 27)** Vol. 3, No. 1, pp. 27. Electronic Publication: 2002-09-27. Journal code: 100965258. E-ISSN: 1471-2164.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: NONMEDLINE; PUBMED-NOT-MEDLINE
ENTRY MONTH: 200310
ENTRY DATE: Entered STN: 20031101
Last Updated on STN: 20031101
Entered Medline: 20031031

AB BACKGROUND: The objective of this research was to investigate the reproducibility of cross-species **microarray** hybridisation. Comparisons between same- and cross-species hybridisations were also made. Nine hybridisations between a single **pig** skeletal **muscle** RNA sample and three human **cDNA** nylon **microarrays** were completed. Three replicate hybridisations of two different amounts of **pig** RNA, and of human skeletal **muscle** RNA were completed on three additional **microarrays**. RESULTS: Reproducibility of **microarray** hybridisations of **pig cDNA** to human **microarrays** was high, as determined by Spearman and Pearson correlation coefficients and a Kappa statistic. Variability among replicate hybridisations was similar for human and **pig** data, indicating the reproducibility of results were not compromised in

cross-species hybridisations. The concordance between data generated from hybridisations using **pig** and human skeletal **muscle** RNA was high, further supporting the use of human **microarrays** for the analysis of gene expression in the **pig**. No systematic effect of stripping and re-using nylon **microarrays** was found, and variability across **microarrays** was minimal. CONCLUSION: The majority of genes generated highly reproducible data in cross-species **microarray** hybridisations, although approximately 6% were identified as highly variable. Experimental designs that include at least three replicate hybridisations for each experimental treatment will enable the variability of individual genes to be considered appropriately. The use of cross-species **microarray** analysis looks promising. However, additional validation is needed to determine the specificity of cross-species hybridisations, and the validity of results.

L6 ANSWER 6 OF 24 MEDLINE on STN
ACCESSION NUMBER: 2003010719 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12517075
TITLE: Generation of expressed sequence tags from a normalized **porcine** skeletal **muscle cDNA** library.
AUTHOR: Yao Jianbo; Coussens Paul M; Saama Peter; Suchyta Steven; Ernst Catherine W
CORPORATE SOURCE: Department of Animal Science and Center for Animal Functional Genomics, Michigan State University, East Lansing, MI 48824, USA.. yaoj@msu.edu
SOURCE: Animal biotechnology, **(2002 Nov)** Vol. 13, No. 2, pp. 211-22.
Journal code: 9011409. ISSN: 1049-5398.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-BM189924; GENBANK-BM189925; GENBANK-BM189926; GENBANK-BM189927; GENBANK-BM189928; GENBANK-BM189929; GENBANK-BM189930; GENBANK-BM189931; GENBANK-BM189932; GENBANK-BM189933; GENBANK-BM189934; GENBANK-BM189935; GENBANK-BM189936; GENBANK-BM189937; GENBANK-BM189938; GENBANK-BM189939; GENBANK-BM189940; GENBANK-BM189941; GENBANK-BM189942; GENBANK-BM189943; GENBANK-BM189944; GENBANK-BM189945; GENBANK-BM189946; GENBANK-BM189947; GENBANK-BM189948; GENBANK-BM189949; GENBANK-BM189950; GENBANK-BM189951; GENBANK-BM189952; GENBANK-BM189953; GENBANK-BM189954; GENBANK-BM189955; GENBANK-BM189956; GENBANK-BM189957; GENBANK-BM189958; GENBANK-BM189959; GENBANK-BM189960; GENBANK-BM189961; GENBANK-BM189962; GENBANK-BM189963; GENBANK-BM189964; GENBANK-BM189965; GENBANK-BM189966; GENBANK-BM189967; GENBANK-BM189968; GENBANK-BM189969; GENBANK-BM189970; GENBANK-BM189971; GENBANK-BM189972; GENBANK-BM189973; GENBANK-BM189974; GENBANK-BM189975; GENBANK-BM189976; GENBANK-BM189977; GENBANK-BM189978; GENBANK-BM189979; GENBANK-BM189980; GENBANK-BM189981; GENBANK-BM189982; GENBANK-BM189983; GENBANK-BM189984; GENBANK-BM189985; GENBANK-BM189986; GENBANK-BM189987; GENBANK-BM189988; GENBANK-BM189989; GENBANK-BM189990; GENBANK-BM189991; GENBANK-BM189992; GENBANK-BM189993; GENBANK-BM189994; GENBANK-BM189995; GENBANK-BM189996; GENBANK-BM189997; GENBANK-BM189998; GENBANK-BM189999; GENBANK-BM190000; GENBANK-BM190001; GENBANK-BM190002; GENBANK-BM190003; GENBANK-BM190004; GENBANK-BM190005; GENBANK-BM190006; GENBANK-BM190007; GENBANK-BM190008; GENBANK-BM190009; GENBANK-BM190010; GENBANK-BM190011; GENBANK-BM190012; GENBANK-BM190013; GENBANK-BM190014; GENBANK-BM190015; GENBANK-BM190016;

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AB Recent developments in **microarray** technologies permit scientists to analyze expression of thousands of genes simultaneously in diverse biological systems. In an effort to provide integrated resources for application of **microarray** technologies to studies of skeletal **muscle** growth and development in **swine**, we have constructed a normalized **cDNA** library from **porcine** skeletal **muscle**. The effectiveness of normalization was evaluated by DNA sequencing of clones randomly picked from the library before and after normalization, and also by Southern blot hybridization using probes representing abundant transcripts. Our data suggests that the normalization procedure successfully reduced the highly abundant **cDNA** species in the normalized library. To date, a total of 782 EST (expressed sequence tag) sequences have been generated from this normalized library (687 ESTs) and the original library (95 ESTs). The sequence information of these ESTs plus their BLAST results has been made available through a web accessible database (http://nbfgc.msu.edu). Cluster analysis of the data indicates that a total of 742 unique sequences are present in this collection. BLASTN search of the 742 EST sequences against the public database (dbEST) revealed that 139 had no significant matches (E-value > 10(-15)) to **porcine** ESTs already entered in the database, suggesting the possibility of their specific expression in **porcine** skeletal **muscle**. Generation of

non-redundant ESTs from this library will allow us to construct **cDNA microarrays** for identification of gene expression changes that regulate **muscle** growth and affect meat quality in **swine**.

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AB Purpose: **Microarray** analysis was used to determine if **porcine cDNA** would hybridize cleanly to human **cDNA arrays**. Gene expression from ocular tissues was measured and compared to help elucidate their functions. It was sought to determine if unique gene upregulation in different ocular tissues occurs, and if so what genes are involved. Methods: Total RNA was extracted from **porcine** iris, cilliary body, retina, and optic nerve tissues. Labeled **cDNA** was generated using the Perkin Elmer TSA kit. Samples were hybridized to human **cDNA microarrays** containing 5700 PCR products spotted in duplicate. Amplicons making up the **arrays** are genes or ESTs, and are amplified from ResGen human library clones. Labeled cilliary body, optic nerve, and retina **cDNA** were each hybridized separately with labeled iris **cDNA** on two double spotted **arrays**. Results: It was found that there are genes which are upregulated uniquely in each of the ocular tissues studied. Cilliary body uniquely upregulated genes included lysyl oxidase - like1 (LOXL1), ATP1 B3 ATPase, Na+/K+ transporting, beta 3 polypeptide, FMOD Fibromodulin, GPNMB Glycoprotein (transmembrane) nmb, and OAT Ornithine aminotrasferase (gyrate atrophy). In Iris Beta A1 Crystallin (CRYBA1), and Actin gamma 2 smooth **muscle** enteric (ACTG2) were uniquely upregulated. Myelin Basic Protein (MBP), Proteolipid protein 1 (PLP1), Myelin - associated oligodendrocyte basic protein (MOBP), and S100 calcium - binding protein beta (SB100) were unique to optic nerve. In Retinal tissue CKMT2 creatine kinase mitochondrial 2 (sarcomeric), UNC119 (c. elegans) homolog, and ATPB2 ATPase Na+/K+ transporting beta 2 polypeptide were found to be uniquely upregulated. Conclusion: Upregulated genes in **porcine** ocular tissues could be determined by **microarray** analysis with SMChum5700 human **cDNA arrays** from the Spotted **Microarray** Core at Oregon Health and Science University. Genes that are upregulated specific to tissue type are able to be determined using these **arrays**.

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